

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/049,695A

1642

DATE: 02/23/2000
TIME: 01:37:53

INPUT SET: S34817.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

1
2
3 (1) General Information
4
5 (i) APPLICANT: BILLING-MEDEL, PATRICIA A.
6 COHEN, MAURICE
7 COLPITTS, TRACEY L.
8 FRIEDMAN, PAULA N.
9 HAYDEN, MARK
10 KCLASS, MICHAEL R.
11 ROBERTS-RAPP, LISA
12 RUSSELL, JOHN C.
13 STROUPE, STEPHEN D.
14
15
16
17 (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
18 FOR DETECTING DISEASES OF THE GASTROINTESTINAL
19 TRACT
20
21 (iii) NUMBER OF SEQUENCES: 25
22
23 (iv) CORRESPONDENCE ADDRESS:
24 (A) ADDRESSEE: Abbott Laboratories
25 (B) STREET: 100 Abbott Park Road
26 (C) CITY: Abbott Park
27 (D) STATE: IL
28 (E) COUNTRY: USA
29 (F) ZIP: 60064-3500
30
31 (v) COMPUTER READABLE FORM:
32 (A) MEDIUM TYPE: Diskette
33 (B) COMPUTER: IBM Compatible
34 (C) OPERATING SYSTEM: DOS
35 (D) SOFTWARE: FastSEQ for Windows Version 2.0
36
37 (vi) CURRENT APPLICATION DATA:
38 (A) APPLICATION NUMBER:
39 (B) FILING DATE:
40 (C) CLASSIFICATION:
41
42 (vii) PRIOR APPLICATION DATA:
43 (A) APPLICATION NUMBER: 08/828,845
44 (B) FILING DATE: 31-MAR-1997
45

Does Not Comply
Corrected Diskette Needed

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PATENT APPLICATION US/09/049,695ADATE: 02/23/2000
TIME: 01:37:54

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46
47 (viii) ATTORNEY/AGENT INFORMATION:
48 (A) NAME: Becker, Cheryl L.
49 (B) REGISTRATION NUMBER: 35,441
50 (C) REFERENCE/DOCKET NUMBER: 6066.US.P1
51
52 (ix) TELECOMMUNICATION INFORMATION:
53 (A) TELEPHONE: 847/935-1729
54 (B) TELEFAX: 847/938-2623
55 (C) TELEX:
56
57

ERRORED SEQUENCES FOLLOW:

433 (2) INFORMATION FOR SEQ ID NO:23:
434
435 (i) SEQUENCE CHARACTERISTICS:
--> 436 (A) LENGTH: 249 base pairs
--> 437 (B) TYPE: DNA *nucleic acid*
438 (C) STRANDEDNESS: single
439 (D) TOPOLOGY: linear
440
441
442 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
443
--> 444 GGATCAGCCA CTGCAGCTCC CTGAGCACTC TCTACAGAGA CGCGGACCCC AGACATGAGG 60
--> 445 AGGCTCCTCC TGGTCACCAG CCTGGTGGTT GTGCTGCTGT GGGAGGCAGG TGCAGTCCCA 120
--> 446 GCACCCAAGG TCCCTATCAA GATGCAAGTC AAACACTGGC CCTCAGAGCA GGACCCAGAG 180
--> 447 AAGGCCTGGG GCGCCCGTGT GGTGGAGCCT CCGGAGAAGG ACGACCAGCT GGTGGTGCTG 240
--> 448 TTCCCTGTC 249
449
450

451 (2) INFORMATION FOR SEQ ID NO:24:
452
453 (i) SEQUENCE CHARACTERISTICS:
--> 454 (A) LENGTH: 336 base pairs
--> 455 (B) TYPE: DNA
456 (C) STRANDEDNESS: single
457 (D) TOPOLOGY: linear
458
459
460 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
461
--> 462 GGCAGGTGCA GTCCCAGCAC CCAAGGTCCC TATCAAGATG CAAGTCAAAC ACTGGCCCTC 60
--> 463 AGAGCAGGAC CCAGAGAAGG CCTGGGGCGC CCGTGTGGTG GAGCCTCCGG AGAAGGACGA 120
--> 464 CCAGCTGGTG GTGCTGTTCC CTGTCCAGAA GCCGAAACTC TTGACCACCG AGGAGAAGCC 180
--> 465 ACGAGGTCAG GGCAGGGGCC CCATCCTTCC AGGCACCAAG GCCTGGATGG AGACCGAGGA 240
--> 466 CACCCTGGGC CGTGTCTCTGA GTCCCGAGCC CGACCATGAC AGCCTGTACC ACCCTCCGCC 300

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--> 467 TGAGGAGGAC CAGGGCGAGG AGAGGCCCCG GTTGTG
468
469

336

470 (2) INFORMATION FOR SEQ ID NO:25:
471
472 (i) SEQUENCE CHARACTERISTICS:
--> 473 (A) LENGTH: 309 base pairs
--> 474 (B) TYPE: DNA
475 (C) STRANDEDNESS: single
476 (D) TOPOLOGY: linear
477
478 (ix) FEATURE:
479 (A) NAME/KEY: base_polymorphism
480 (B) LOCATION: 8
481 (D) OTHER INFORMATION: /note= "'N' represents an A or G or
482 T or C polymorphism at this position"
483
484 (ix) FEATURE:
485 (A) NAME/KEY: base_polymorphism
486 (B) LOCATION: 102
487 (D) OTHER INFORMATION: /note= "'N' represents an A or G or
488 T or C polymorphism at this position"
489
490 (ix) FEATURE:
491 (A) NAME/KEY: base_polymorphism
492 (B) LOCATION: 194
493 (D) OTHER INFORMATION: /note= "'N' represents an A or G or
494 T or C polymorphism at this position"
495
496 (ix) FEATURE:
497 (A) NAME/KEY: base_polymorphism
498 (B) LOCATION: 212
499 (D) OTHER INFORMATION: /note= "'N' represents an A or G or
500 T or C polymorphism at this position"
501
502 (ix) FEATURE:
503 (A) NAME/KEY: base_polymorphism
504 (B) LOCATION: 225
505 (D) OTHER INFORMATION: /note= "'N' represents an A or G or
506 T or C polymorphism at this position"
507
508 (ix) FEATURE:
509 (A) NAME/KEY: base_polymorphism
510 (B) LOCATION: 230
511 (D) OTHER INFORMATION: /note= "'N' represents an A or G or
512 T or C polymorphism at this position"
513
514 (ix) FEATURE:
515 (A) NAME/KEY: base_polymorphism
516 (B) LOCATION: 259
517 (D) OTHER INFORMATION: /note= "'N' represents an A or G or
518 T or C polymorphism at this position"

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519
520
521 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
522
--> 523 G C C C C A T N C T T C C A G G C A C C A A G G C C T G G A T G G A G A C C G A G G A C A C C C T G G G C C G T G T C C 60
--> 524 T G A G T C C C G A G C C C G A C C A T G A C A G C C T G T A C C A C C C T C C G N C T G A G G A G G A C C A G G G C G 120
--> 525 A G G A G A G G C C C C G G T T G T G G G T G A T G C C A A A T C A C C A G G T G C T C C T G G G A C C G G A G G A A G 180
--> 526 A C C A A G A C C A C A T N T A C C A A C C C C A G T A G G G N T T C A G G G G C C A T N A G T G N C C C C G G C C T G 240
--> 527 T T C C A A G G C C C A G G T G T T N G G A T T G G A C C T T C C T A A C C T G C C C A G T T A G A C A A T A A A A C 300
528

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/049,695ADATE: 02/23/2000
TIME: 01:37:55

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Line	Error	Original Text
436	Entered (249) and Calc. Seq. Length (0) differ	(A) LENGTH: 249 base pairs
437	Wrong or Missing Sequence Type	(B) TYPE: DNA
444	Wrong Amino Acid Designator	GGATCAGCCA CTGCAGCTCC CTGAGCACTC TCTAC
444	Wrong Amino Acid Designator	GGATCAGCCA CTGCAGCTCC CTGAGCACTC TCTAC
444	Wrong Amino Acid Designator	GGATCAGCCA CTGCAGCTCC CTGAGCACTC TCTAC
444	Wrong Amino Acid Designator	GGATCAGCCA CTGCAGCTCC CTGAGCACTC TCTAC
444	Wrong Amino Acid Designator	GGATCAGCCA CTGCAGCTCC CTGAGCACTC TCTAC
444	Wrong Amino Acid Designator	GGATCAGCCA CTGCAGCTCC CTGAGCACTC TCTAC
445	Wrong Amino Acid Designator	AGGCTCCTCC TGGTCACCAG CCTGGTGGTT GTGCT
445	Wrong Amino Acid Designator	AGGCTCCTCC TGGTCACCAG CCTGGTGGTT GTGCT
445	Wrong Amino Acid Designator	AGGCTCCTCC TGGTCACCAG CCTGGTGGTT GTGCT
445	Wrong Amino Acid Designator	AGGCTCCTCC TGGTCACCAG CCTGGTGGTT GTGCT
445	Wrong Amino Acid Designator	AGGCTCCTCC TGGTCACCAG CCTGGTGGTT GTGCT
445	Wrong Amino Acid Designator	AGGCTCCTCC TGGTCACCAG CCTGGTGGTT GTGCT
446	Wrong Amino Acid Designator	GCACCCAAGG TCCCTATCAA GATGCAAGTC AAACA
446	Wrong Amino Acid Designator	GCACCCAAGG TCCCTATCAA GATGCAAGTC AAACA
446	Wrong Amino Acid Designator	GCACCCAAGG TCCCTATCAA GATGCAAGTC AAACA
446	Wrong Amino Acid Designator	GCACCCAAGG TCCCTATCAA GATGCAAGTC AAACA
446	Wrong Amino Acid Designator	GCACCCAAGG TCCCTATCAA GATGCAAGTC AAACA
447	Wrong Amino Acid Designator	AAGGCCTGGG GCGCCCGTGT GGTGGAGCCT CCGGA
447	Wrong Amino Acid Designator	AAGGCCTGGG GCGCCCGTGT GGTGGAGCCT CCGGA
447	Wrong Amino Acid Designator	AAGGCCTGGG GCGCCCGTGT GGTGGAGCCT CCGGA
447	Wrong Amino Acid Designator	AAGGCCTGGG GCGCCCGTGT GGTGGAGCCT CCGGA
447	Wrong Amino Acid Designator	AAGGCCTGGG GCGCCCGTGT GGTGGAGCCT CCGGA
447	Wrong Amino Acid Designator	AAGGCCTGGG GCGCCCGTGT GGTGGAGCCT CCGGA
448	Wrong Amino Acid Designator	TTCCCTGTC
454	Entered (336) and Calc. Seq. Length (0) differ	(A) LENGTH: 336 base pairs
455	Wrong or Missing Sequence Type	(B) TYPE: DNA
462	Wrong Amino Acid Designator	GGCAGGTGCA GTCCCAGCAC CCAAGGTCCC TATCA
462	Wrong Amino Acid Designator	GGCAGGTGCA GTCCCAGCAC CCAAGGTCCC TATCA
462	Wrong Amino Acid Designator	GGCAGGTGCA GTCCCAGCAC CCAAGGTCCC TATCA
462	Wrong Amino Acid Designator	GGCAGGTGCA GTCCCAGCAC CCAAGGTCCC TATCA
462	Wrong Amino Acid Designator	GGCAGGTGCA GTCCCAGCAC CCAAGGTCCC TATCA
462	Wrong Amino Acid Designator	GGCAGGTGCA GTCCCAGCAC CCAAGGTCCC TATCA
463	Wrong Amino Acid Designator	AGAGCAGGAC CCAGAGAAGG CCTGGGGCGC CCGT
463	Wrong Amino Acid Designator	AGAGCAGGAC CCAGAGAAGG CCTGGGGCGC CCGT
463	Wrong Amino Acid Designator	AGAGCAGGAC CCAGAGAAGG CCTGGGGCGC CCGT
463	Wrong Amino Acid Designator	AGAGCAGGAC CCAGAGAAGG CCTGGGGCGC CCGT
463	Wrong Amino Acid Designator	AGAGCAGGAC CCAGAGAAGG CCTGGGGCGC CCGT
463	Wrong Amino Acid Designator	AGAGCAGGAC CCAGAGAAGG CCTGGGGCGC CCGT
464	Wrong Amino Acid Designator	CCAGCTGGTG GTGCTGTTCC CTGTCCAGAA GCCGA
464	Wrong Amino Acid Designator	CCAGCTGGTG GTGCTGTTCC CTGTCCAGAA GCCGA
464	Wrong Amino Acid Designator	CCAGCTGGTG GTGCTGTTCC CTGTCCAGAA GCCGA
464	Wrong Amino Acid Designator	CCAGCTGGTG GTGCTGTTCC CTGTCCAGAA GCCGA
464	Wrong Amino Acid Designator	CCAGCTGGTG GTGCTGTTCC CTGTCCAGAA GCCGA
465	Wrong Amino Acid Designator	ACGAGGTCAG GGCAGGGGCC CCATCCTTCC AGGCA

INPUT SET: S34817.raw[illegible]